

ICR Wiki Home Page

Useful Links
<ul style="list-style-type: none">• Molecular Analysis Tools Knowledge Center<ul style="list-style-type: none">• caArray• caIntegrator• GenePattern• geWorkbench• Bioconductor• caB2B• caBIO• caLIMS2• caMOD• caNanoLab• Cancer Gene Index• DWD• GeneConnect• gridPIR• LabKey/CPAS• TCGA• Work Products

ICR Active Working Groups
<ul style="list-style-type: none">• Information Representation (IRWG)• Nanotechnology (Nano)

Previous ICR Working Groups
<ul style="list-style-type: none">• Analytical Services Best Practices (ASBP)• ICR Interoperability (ICRi)• Workflow (WFWG)

The Integrative Cancer Research Workspace is producing modular and interoperable tools and interfaces that provide for integration between biomedical informatics applications and data. This will ultimately enable translational and integrative research by providing for the integration of clinical and basic research data. The Workspace is developing a software-engineered, well-documented and validated biomedical informatics toolset for use throughout the research community.

Additional information is also found on the [Molecular Analysis Knowledge Center](#) site.

Open Development and Community Projects Speaker Series



ICR WS Teleconference Speakers

The Integrative Cancer Research (ICR) Workspace is hosting a series of speakers on various open development and community driven projects. While the applications may be of greatest interest to ICR, the conversations about success factors for these types of projects is of general interest to the caBIG community. Meeting minutes are posted below.

You are welcome to join us on the 2nd and 4th Wednesdays of each month from 2:00 – 4:00 pm ET. Teleconference information:

800-593-0616 passcode: 2927756.

Adobe connect: <http://cbit.acrobat.com/icrws/>

- June 22
 - BioPAX and GeneMANIA; Gary Bader, U. of Toronto
 - I SPY/ Transcend; Sarah Davis, UCSF
- July 13
 - Protein Ontology; Cecilia Neomi Arighi, U. of Delaware
 - Data standards and the Cardiovascular DAM at Duke University; Sal Mungal, Duke University
- July 27
 - SBML: Systems Biology Markup Language – Mike Hucka, California Institute of Technology
- Aug 24
 - HL7 Clinical Genomics Working Group: Amnon Shabo, Head of the Healthcare and Life Sciences Standards Program, IBM
- Sept 14
 - eagle-I consortium and their research resource discovery network for biomedical scientists: Carlo Torniai, Oregon Health and Science University
 - GMOD (**G**eneric **M**odel **O**rganism **D**atabase) project: Scott Cain, The Ontario Institute for Cancer Research
- Sept 28
 - NCBO Organization and Outreach; Ray Fergerson - NCBO Project Director, Stanford University
- Oct 12
 - GenomeSpace – Michael Reich, Broad Institute
- Oct 26
 - OBI (The Ontology for Biomedical Investigations), an international project developing an integrated ontology for the description of life-science and clinical investigations. - Jennifer Fostel, NIEHS

Recent News



New Article: Informatics and Standards for Nanomedicine Technology

A recent focus article in "Wiley Interdisciplinary Reviews: Nanomedicine and Nanobiotechnology," explores nanotechnology and its impact on medicine and biomedical research, as well as the need for informatics standards in Nanomedicine. To read more about how Nanotechnology has the potential to make medicine more personalized, predictive, and preemptive, [click here](#).



Nanotechnology Expert Dr. Stacey Harper Awarded \$1.9 Million NIEHS Grant

This new, five-year grant will provide extended research support to allow Dr. Harper of Oregon State University to continue to develop one of the nation's leading programs to test the safety of compounds created through nanotechnology. While Dr. Harper has many credits to her name and too many accomplishments to list here, we want to congratulate her on this latest achievement, and we look forward to continuing to work with Dr. Harper through the caBIG[®] Nanotechnology Working Group. Please join us in congratulating Dr. Harper on this truly outstanding achievement and wish her continued success in her research endeavors.

Teleconference Materials

The meeting **Date** is hyperlinked to the notes and hyperlinks in the **Executive Summary** are for specific presentations

Date	Executive Summary
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October 12, 2011	<ul style="list-style-type: none"> • Sherri Decoronado (no slides) spoke about the NCI Provocative Questions. This is a list of important but non-obvious questions that will stimulate the NCI's research communities to use laboratory, clinical, and population sciences in especially effective and imaginative ways. • Zhong Li highlighted the new Molecular Analysis Tools Knowledge Center wiki which provides centralized, authoritative repository of knowledge, information, and web-based support to facilitate the deployment and ongoing development of caBIG® tools, standards, and infrastructure in the molecular analysis domain. Tools supported are caArray, caIntegrator, GenePattern and geWorkbench. • Rashmi Srinivasa provided an update on caArray, the array data management system. • Michael Reich (slides on request efreund@3rdmill.com) presented GenomeSpace, a community space for creating and sharing genomic analysis tools (It is seeded with six popular genomics tools (Cytoscape, Galaxy, GenePattern, Genomica, Integrative Genomics Viewer (IGV), and the UCSC Browser).
September 28, 2011	<p>Dr. Ray Ferguson is from the Stanford Center for Biomedical Informatics Research and is the NCBO Project Director. He is one of the developers of the Protégé OWL plugin. He spoke about the NCBO organization, outreach and factors for success.</p> <p>Mukesh Sharma (no slides) from Washington University at St. Louis is the IRWG Liaison to the HL7 Clinical Genomics Work Group (HL7 CG WG). He reported in on the HL7 CG WG F2F meeting held in the context of the HL7 meeting in San Diego.</p>
September 14, 2011	<p>Carlo Torniai, an ontologist from Oregon Health and Science University, spoke on the eagle-I consortium and their research resource discovery network for biomedical scientists.</p> <p>Scott Cain, from The Ontario Institute for Cancer Research, presented the GMOD (Generic Model Organism Database) project. GMOD is a collection of interoperable open source software tools for creating and managing genome-scale biological databases, including individual or web-accessible database creation, visualizing, annotation.</p> <p>Baris Suzek from Georgetown University reported on the recent meeting "Crowdsourcing: The Art and Science of Open Innovation"</p>
August 24, 2011, 2-4 PM Eastern	<p>Amnon Shabo (slides on request efreund@3rdmill.com) spoke about the HL7 Clinical Genomics Work Group - From Healthcare to Research.</p>
July 27, 2011, 2-4 PM Eastern	<p>Mike Hucka (slides on request efreund@3rdmill.com) from Caltech spoke about SBML (Systems Biology Markup Language) as an open community standard initiative. SBML is a representation format, based on XML, for communicating and storing computational models of biological processes. Mike reviewed past, present and future directions for the community and provided lessons learned – what went right (involved actual stakeholders, addressed real needs -not perceived ones, transparent and inclusive process, etc.) and where there were challenges (testing, complexity creep, not formalizing processes sufficiently).</p>
July 13, 2011, 2-4 PM Eastern	<p>Cecilia Neomi Arighi from U of Delaware presented on Protein Ontology. (PRO) provides the ontological representation of proteins and protein complexes and shows the relationships between them. It encompasses three sub-ontologies: proteins based on evolutionary relatedness (ProEvo); protein forms produced from a given gene locus (ProForm); and protein-containing complexes (ProComp). There is a website with extensive browse and search capabilities and includes additional annotations using other ontologies like Pfam and GO.</p> <p>Sal Mungai of Duke University talked about his work on promoting interoperability through the creation of a cardiovascular domain analysis model. This will be a component of their initiative to streamline all data collection and analysis through integration of data, annotations and analytical tools. The cardiovascular DAM uses at</p>
June 22, 2011, 2-4 PM Eastern	<ul style="list-style-type: none"> • Gary Bader gave a presentation on BioPAX, a standard language that enables integration, exchange, visualization and analysis of biological pathway data. BioPAX underlies the integration of public database content in Pathwaycommons.org, which has a comprehensive directory of interaction and pathway databases as well as search, download and visualization tools (from Cytoscape). Dr. Bader also gave a demo of GeneMANIA, a tool to predict gene function, gene sets, pathway members, complexes etc. It draws data from Pathway Commons and uses a Cytoscape webservice for visualization. Pathway Commons and GeneMANIA (and Cytoscape) are built entirely on open source software. • Sarah Davis (slides on request efreund@3rdmill.com) spoke about the I-SPY 2 TRIAL. It is a breast cancer adaptive clinical trial which uses a different (neoadjuvant) approach allowing them to: determine new therapeutic efficacy on a much shorter time scale; use findings to assign patients to appropriate treatment arms of the trial. The need to integrate molecular and imaging data from consortium participants required a new bioinformatics infrastructure known as TRANSCEND which makes use of several caBIG tools.
June 8, 2011, 2-4 PM Eastern	<p>John Speakman, NCI CBIIT CPO kicked-off the workspace call with a caBIG Program Update. Mike Smoot, UCSD, is lead developer for Cytoscape. He provided an overview of the Cytoscape software platform for visualizing molecular interactions and pathways and integrating these with annotations and data. His talk also focused on the active Cytoscape community.</p> <p>Sunny Jansen is a researcher at the Mouse Cancer Genetics Program on the Ft. Detrick campus in Maryland. She is doing a mouse GBM study using caBIG tools such as NBIA and caIntegrator with imaging, pre-clinical and genomic data.</p> <p>RaviSlidesGalaxyConference508.pptx</p> <p>Ravi Madduri from Argonne National Lab will provide an update on his work with Galaxy. He was recently in the Netherlands at the Galaxy users meeting and presented his work on highthroughput data and identity management in Galaxy.</p>

May 25, 2011, 2-4 PM Eastern	<p>Mark Bray from the Broad Institute gave a presentation on CellProfiler. It is a tool which integrates various algorithms. It is capable of extracting measurements for every individual cell in an image-based screen, ranging from standard assays (e.g., cell count, size, per-cell protein levels) as well as more complex morphological assays (e.g., cell/organelle shape or subcellular patterns of DNA or protein staining).</p> <p>Judith Blake from the Jackson Laboratory discussed the Gene Ontology (GO). GO provides a standardized representation of gene and gene product attributes and is comprised of a controlled vocabulary, gene product annotation data and tools to access and process the data (GO Browser and OBO ontology editor). GO is maintained by the GO Consortium which is comprised of organism and protein databases and the biological research community.</p>
May 11, 2011, 2-4 PM Eastern	<ul style="list-style-type: none"> • Rashmi Srinivasa hosted a caArray Users Meeting. She discussed features of the upcoming 2.4.1 release and the plans for the following release. • Grace Stafford provided an update on The Jackson Laboratory caBIG Deployment Implementation. This included the impact of next generation sequencing technologies on the computational core tool needs and requirements emerging from new projects. • Ravi Madduri (no slides) provided a demonstration of caBIG workflows run using the Galaxy platform.
April 27, 2011, 2-4 PM Eastern	<p>The ICR workspace heard reports on the recent BioIT and AACR meetings from Mark Adams (BAH) and Jens Poschet (Sapient) respectively.</p> <p>Jason Hipp of University of Michigan gave a presentation on the use of Laser Capture Microdissection in --omics research.</p>
April 13, 2011, 2-4 PM Eastern	<p>The ICR participants presented on their assigned projects.</p> <p>Jim McCusker, caIntegrator Community Contribution of Code, discussed his implementation experience and future recommendations.</p> <p>Dennis Thomas, Extending the Use of the NanoParticle Ontology, addressed challenges for using NPO with nano-TAB and caNanoLab NPO for data annotation, semantic integration of data, unambiguous interpretation and data sharing.</p> <p>Mukesh Sharma, HL7 Clinical Genomics WG, discussed "Considering changing mission and charter to reflect changing technology" and "Mission to include bridging semantics between clinical and research domains."</p> <p>Nathan Baker reviewed the updates and future goals of the Nanotechnology Working Group.</p> <p>Bob Freimuth, Information Representation Working Group, reviewed the activities and future recommendations for the period.</p>
March 23, 2011, 2-4 PM Eastern	<p>Alex Kanous from the DSIC Knowledge Center provided a presentation on the electronic Data Use Agreement tool. The tool may be used for generating DUAs for outgoing data based on a catalog of standardized, modular contract clauses, each of which corresponds to one of the E-DSSF's sensitivity ratings.</p> <p>Joshua Phillips and Ravi Madduri discussed the prototyping activities on workflows for caGrid 2.0. They described use cases and requirements for workflows, defining metadata needed for discovery, composition, and execution of workflows and their consideration of how best to use W3C technologies (e.g. RDF, SPARQL, SA-WSDL, inference). They also provided a demo of a workflow engine prototype based on SADI and Taverna.</p> <p>Ken Quinn spoke about the Roswell Park deployment of caGrid technology and use of caB2B to do federated queries across disparate, decentralized heterogeneous databases and clinical systems to support non-interventional clinical research. He described the process and challenges including: gathering senior leadership support, understanding the myriad research databases, gaining technical expertise, lack of common vocabularies and the excellent collaboration and support provided by the caB2B knowledge center.</p>
February 23, 2011, 2-4 PM Eastern	<p>Anton Nekrutenko and Daniel Blankenberg and of The Pennsylvania State University gave a presentation on Galaxy, an open-source next generation sequence (NGS) analysis software system. It addresses the need to empower the scientists without access to extensive infrastructure to do the analysis. Galaxy is a free web service, and has a plethora of analysis tools and has workflow generation capabilities</p> <p>Stacey Harper gave a briefing on nano-TAB, a general purpose framework that provides a standard means to communicate nanomaterial data and metadata. The needs the data exchange format addresses and an overview of the file structure were discussed.</p>
February 14, 2011, 2-4 PM Eastern	<p>caArray Users Meeting featured upcoming plugin architecture for support the addition of new parsers and data storage mechanisms.</p>
January 26, 2011, 2-4 PM Eastern	<p>Jenny Kelley, NCI Population Sciences, updated the community on caLIMS v2 new features. She also provided a thorough demonstration of the tool.</p> <p>The details on the upcoming release of caB2B in March were presented by Baris Suzek of Georgetown University. The tool will assist Bioinformaticians and Researchers discover and collect data on the Grid.</p> <p>Nano WG and LS SME WG each presented an overview and current goals to the community.</p>
January 12, 2011, 2-4 PM Eastern	<p>The ICR Workspace is hearing reports on activities for the last period.</p> <ul style="list-style-type: none"> • Bob Freimuth discussed IRWG work on the LS DAM Updates and additions to the model will appear in the next release. Work on the portion of the model shared with HL7 Clinical Genomics Working Group is extending the generic assay core to include concepts for gene variation. • Dennis Thomas reported on the processes to integrate the NanoParticle Ontology into the NCI Metathesaurus. This expands NPO accessibility and brings more semantics into the NCImt.

Looking for older notes? [Access ICR Meeting Notes Archive](#)

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HL7 Clinical Genomics Work Group – From Research to Healthcare